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PATENT
Attorney Docket No.: 02307E-114910US
Client Ref. No.: 2001-124-2

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

On April 28, 2005

TOWNSEND and TOWNSEND and CREW LLP

By: Patricia Anders

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Zuker et al.

Application No.: 10/026,188

Filed: December 21, 2001

For: ASSAYS FOR TASTE RECEPTOR
CELL SPECIFIC ION CHANNEL

Customer No.: 20350

Confirmation No. 9521

Examiner: Michael T. Brannock

Technology Center/Art Unit: 1646

Declaration of Charles S. Zuker and Yifeng

Zhang pursuant to 37 C. F. R. §1.131

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

We, Charles S. Zuker and Yifeng Zhang, being duly warned that willful false statements and the like are punishable by fine or imprisonment or both, under 18 U.S.C. §1001, and may jeopardize the validity of the patent application or any patent issuing thereon, state and declare as follows:

1. All statements herein made of our own knowledge are true and statements made on information or belief are believed to be true. Exhibits I-V are attached hereto and incorporated herein by reference.

2. At the time this invention was first conceived, we were employees of Howard Hughes Medical Institute and the University of California, located in San Diego, California. All activities described in this Declaration took place in the United States of America.

3. In accordance with 37 C.F.R. §1.131, we state that we completed the claimed invention in the United States prior to April 17, 2000, the filing date of USSN 60/197,491, to which published U.S. Patent Application US 2002/0037515 claims priority.

4. Attached to this Declaration are:

Exhibit I, pages of a printout of a sequence file containing the polynucleotide sequence of 930 clones obtained from a subtracted cDNA library prepared from rat circumvallate cells, following the experimental procedure described in Example I of the application. The pages of Exhibit I indicate the date of last modification to contiguous sequence ("contig") No. 068-3 157 501 and the polynucleotide sequence of clone 501, one of the three clones that make up this contig;

Exhibit II, pages of laboratory notebook indicating that a Blast search was performed for known polynucleotide sequences matching each one of the 930 clones, including clone 501;

Exhibit III, results of sequence alignment between the mouse Trpm5 (also known as Mtr1 and Ltrpc5) and clone 501, which indicate a high degree of homology;

Exhibit IV, polynucleotide sequences of the mouse Trpm5 (GenBank No. NM_020277, derived from GenBank No. AJ271092, see page 2 of printout for NM_020277) and human Mtr1 (GenBank No. AF177473), which indicate that these sequences were publicly accessible by January 14, 2000 (see page 1 of printout for AJ271092) and August 13, 1999 (see page 1 of printout for AF177473), respectively. Exhibit IV further includes results of a sequence alignment between the amino acid sequences encoded by mouse Trpm5 gene and human Mtr1 gene; and

Exhibit V, results of an *in situ* hybridization experiment indicating the taste cell-specific expression of the gene from which clone 501 is derived, using a nucleic acid probe specific for clone 501, which was also referred to as 501-PCR46. Some dates in the Exhibits have been redacted. All redacted dates in the Exhibits are prior to April 17, 2000.

5. Conception of the present invention as well as its reduction to practice are evidenced by Exhibits I-IV. The first page of Exhibit I shows that contig No. 068-3 157 501 consists of three clones: 3, 157, and 501, the longest of which is clone 501. The second page shows the polynucleotide sequence of clone 501. The third page establishes the time of last modification made to contig No. 068-3 157 501 and therefore establishes the time when the sequence of clone 501 was determined. Upon determination of the polynucleotide sequence of clone 501, a Blast search was conducted to identify known polynucleotide sequence(s) with high level of sequence homology with clone 501. This is evidenced by Exhibit II.

6. The identification of the mouse Trpm5 gene through this sequence homology-based search is evidenced by Exhibit III, which demonstrates that the mouse Trpm5 and clone 501 are highly homologous. Therefore, one of skill in the art would consider the rat gene from which clone 501 is derived to be the ortholog of mouse Trpm5. Although this particular sequence alignment shown in Exhibit III was performed at the present time, the same result would have been (and was indeed) obtained at the time the initial Blast search was performed. This is because, as evidenced by Exhibit IV, the polynucleotide sequence of mouse Trpm5 was publicly accessible well before April 17, 2000. Furthermore, Exhibit IV establishes that human Mtr1 and mouse Trpm5 have a greater than 84% identity in amino acid sequence. Based on this high level of sequence homology, one of skill in the art would recognize human Mtr1 as the ortholog of mouse Trpm5. In addition, Exhibit IV also demonstrates that the polynucleotide sequence of human Mtr1 gene was publicly available well before April 17, 2000. Thus, a Blast search based on the sequence of clone 501 by the present inventors at the time indicated by Exhibit II necessarily led to the identification of both the human and mouse versions of the Mtr1 gene. Subsequently, *in situ* hybridization was performed to confirm the taste cell-specific expression of the rat version of this gene, shown in Exhibit V. It is therefore established that,

Appl. No. 10/026,188
Declaration under 37 C.F.R. §1.131
Reply to Office Action of November 30, 2004

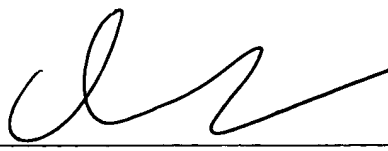
PATENT

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.

7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

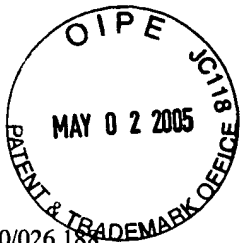
Dated: 4/13/05

By: 
Charles S. Zuker, Ph.D.

Dated: _____

By: _____
Yifeng Zhang, Ph.D.

Attachments (Exhibits I-V)
60427031 V1



Appl. No. 10/026,188
Declaration under 37 C.F.R. §1.131
Reply to Office Action of November 30, 2004

PATENT

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.


7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

Dated: _____

By: _____
Charles S. Zuker, Ph.D.

Dated: 4/20/05

By: 
Yifeng Zhang, Ph.D.

Attachments (Exhibits I-V)
60427031 V1

Rat Sub Seq 12/99 copy
Sequencher™ "Rat Sub Seq 12/99 copy"

Name	Size	Kind	Label	Last Modified
042 GS	205 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:58:
043 GS	392 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
044 86	700 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:44:
045	284 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:33:
046 GS	486 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
047	192 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
048 GS	256 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:00:
049 262-5 GS	408 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:07:
050 120 659	571 BPs	Contig of 3	-	Thu, Feb 3, 2000 8:14:
051 854	350 BPs	Contig of 2	-	Thu, Feb 3, 2000 8:14:
052	603 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
053 3'	105 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:32:
053-5 487-5 GS	309 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:49:
053mid 303	268 BPs	Contig of 2	-	Wed, Jan 19, 2000 6:19:
054	502 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:32:
054 5' ok	102 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:09:
055 3' ok	156 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:09:
055 5'	544 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:31:
056	87 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
057 76 178 464 515-...	252 BPs	Contig of 7	-	Thu, Feb 3, 2000 11:11:
059	330 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
060 895-3 ok	307 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:11:
061	43 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
062	453 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
063 GS	222 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:13:
064	609 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
065 3'	85 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:31:
066 5' ok	541 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:16:
067	580 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
068 5' ok	117 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:17:
068-3 157 501	629 BPs	Contig of 3	-	
069 GS	209 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:19:
070 493-5 648-5	351 BPs	Contig of 3	-	Thu, Feb 3, 2000 11:11:
071	560 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
072 3'	104 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:30:
072 5'	578 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:30:
073 815-3	544 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:49:
074 GS	439 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:20:
075 510 229 831 88...	322 BPs	Contig of 6	-	Wed, Jan 19, 2000 6:19:
078 GS	587 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:22:

Differential Screening + Sequencing

Colony lifts w/ blue-white selection

Hybond N+ lifts

autoclave 5'

rinse to get rid of the debris

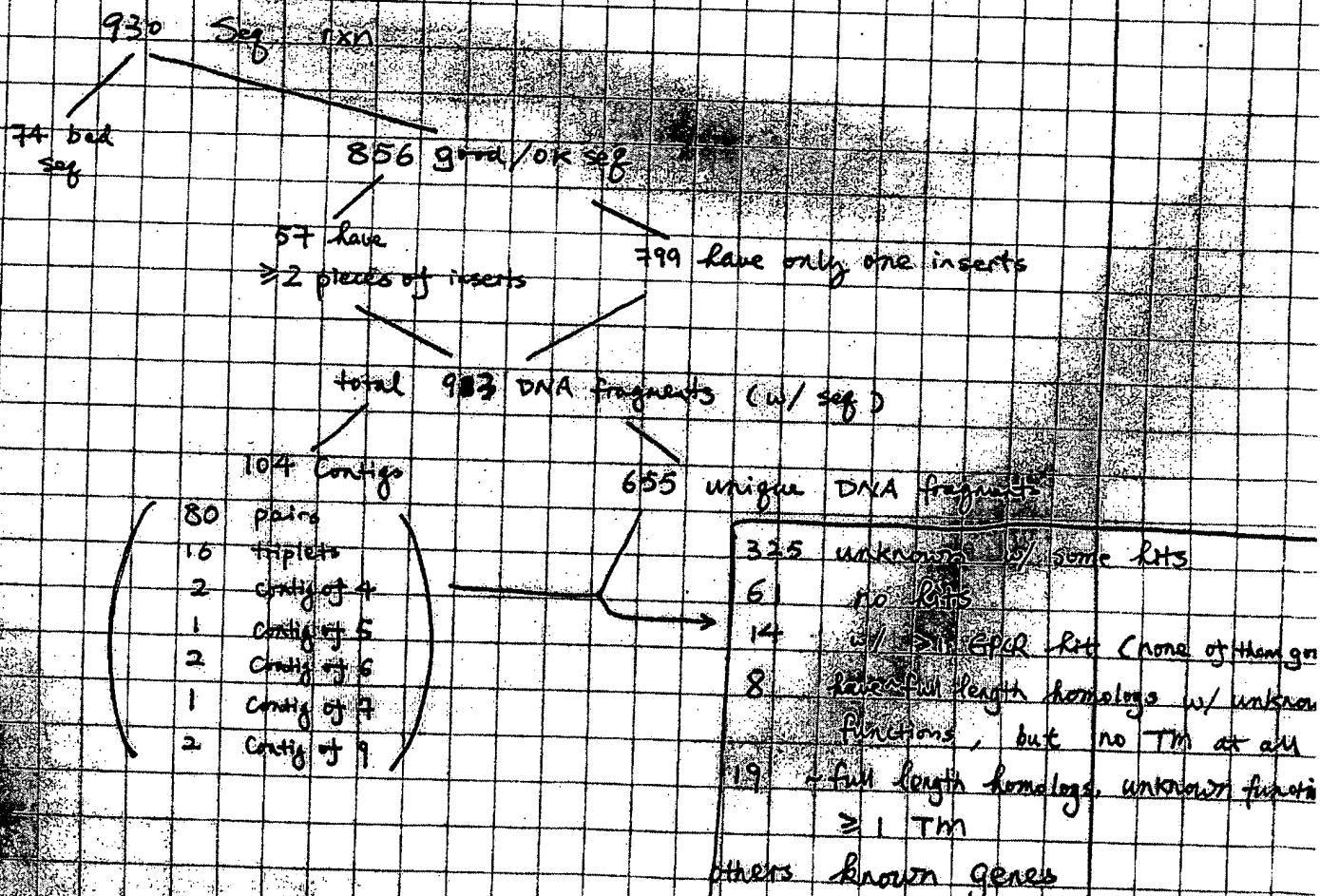
Hyb: w/ sub - (reverse subtracted) as probe

Pick white
Unlighted-up colonies (930)

Miniprep (Clontech 96)

Sequencing (5µl of each DNA sample)

Report



(Continued)

II. SF-615 ~~Env~~ Assay

Not Working !!

Cell lines tried

① Peak Rapid Rb Gx15

② Peak Rapid

See Pg 11 for general info.

A. Blast

Initiator Concentration (M)	(a) \circ Polymerization Rate (g/hr)	(b) \square Polymerization Rate (g/hr)	(c) \triangle Polymerization Rate (g/hr)	(d) \diamond Polymerization Rate (g/hr)
0	0.95	0.85	0.75	0.65
150	0.85	0.75	0.65	0.55
300	0.75	0.65	0.55	0.45
450	0.65	0.55	0.45	0.35
600	0.55	0.45	0.35	0.25
750	0.45	0.35	0.25	0.15
900	0.35	0.25	0.15	0.05



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

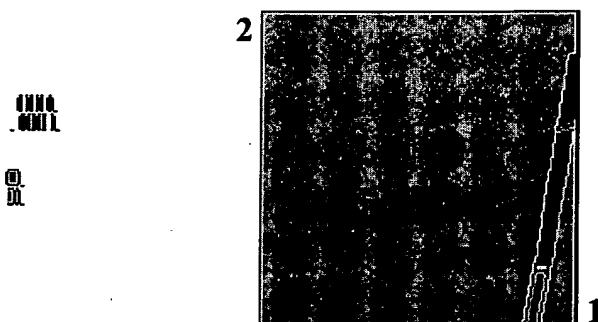
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: **1** Mismatch: **-2** gap open: **5** gap extension: **2**
x dropoff: **50** expect: **10.0** wordsize: **11** Filter **Align**

Sequence 1	gi <u>12383053</u>	Mus musculus transient receptor potential cation channel, subfamily M, member 5 (Trpm5), mRNA	Length 4032 (1 .. 4032)
Sequence 2	lcl 501	contig	Length 627 (1 .. 627)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 371 bits (193), Expect = 7e-99
Identities = 349/414 (84%), Gaps = 9/414 (2%)
Strand = Plus / Plus

11-11-11 11-11-11 11-11-11 11-11-11

```
Query: 3583 ccttgctacagatcacttcttggacatcccttcttaagagaatgaaactcatgtcttttg 3642
          |||||  |||  |  |||||  |  |||||  ||  |||  |||||  |||||
Sbjct: 127  ccttgccgcagaccatgtcttggacacctcttcttatgaaaatgagactcatgtcttttg 186
```

```
Query: 3643 catctattcgggagcctcagaagtatcctctccagcagggcaagatttttcatgtcccac 3702
          ||||| ||||| || || ||||| ||||| || || ||||| ||
Sbjct: 187 catctatctgggagccccaggcgt--cctctccagcagggggaagttttctcatgtcctac 244
```

Query: 3703 -taaagcttttactggttgactggacagctggatctggccaagtcctacataggacac 3761

Sbjct: 245 ctaaaacttttcaccagctaagactggacagctggaactggccaagtcccacatgggatac 304

Query: 3762 catctgcctggatggggctatttaggtctaaccctgtcttaccctgagttcctaagaag 3821
|||||
Sbjct: 305 catctgcctggatggggctacttacgtctagcc--tgtcttaccctgagttccaaagagg 362

Query: 3822 ccaacctcttaaacactag--gtttctttct-gaccctgaccactcattagctgacca 3878
|||||
Sbjct: 363 ccaacctcttaaacactagaggtttccttctgtcctctgatccatccatcagccgacca 422

Query: 3879 gctcctagagggcaggactcagatctattgtaattacctcccatctttcaccctccacag 3938
|||
Sbjct: 423 gcttctagagggcaggactcagatctactgtaatcagctcccatccttcagctccacag 482

Query: 3939 cattatctgtctgatcattctggca-gaaaccccaagatattgctcaaggggtac 3991
|||
Sbjct: 483 cataatttgtgtgatygctcctggcacaaaaccccaagatactgytcaaggggtac 536

Score = 160 bits (83), Expect = 3e-35
Identities = 114/127 (89%), Gaps = 1/127 (0%)
Strand = Plus / Plus



Query: 3442 acctagagtctggcttgccaccctctgacacctgaaatggagaaaccacttgctctagag 3501
|||||
Sbjct: 1 acctagaggctggcttgccacactcagacacctgaaatggagaaaccacttgccctagag 60

Query: 3502 cccagacctggccacatcgagtttttggggcacatcaaccttccccactcccagcagc 3561
|
Sbjct: 61 ctccagacctggccagattgaggttttgggtcacatcaaccttcccctgc-cccagcagc 119

Query: 3562 cccaaga 3568
|||
Sbjct: 120 cccgaga 126

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 1
Number of Hits to DB: 69
Number of extensions: 11
Number of successful extensions: 8
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 4032
Length of database: 13,373,181,452
Length adjustment: 27
Effective length of query: 4005
Effective length of database: 13,373,181,425
Effective search space: 53559591607125
Effective search space used: 53559591607125
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)



5' Nucleotide 3'

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Books

Search for

Limits

Preview/Index

History

Clipboard

Details

GenBank

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD
☒ MGC ☐ HPRD

☐ 1: NM_020277. Reports *Mus musculus* tran...[gi:12383053][Links](#)

LOCUS NM_020277 4032 bp mRNA linear ROD 26-OCT-2004
DEFINITION *Mus musculus* transient receptor potential cation channel, subfamily M, member 5 (Trpm5), mRNA.
ACCESSION NM_020277
VERSION NM_020277.1 GI:12383053
KEYWORDS
SOURCE *Mus musculus* (house mouse)
ORGANISM *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4032)
AUTHORS Liu,D. and Liman,E.R.
TITLE Intracellular Ca²⁺ and the phospholipid PIP₂ regulate the taste transduction ion channel TRPM5
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (25), 15160-15165 (2003)
PUBMED 14657398
REMARK GeneRIF: regulation of TRPM5 by Ca²⁺ mediates sensory activation in the taste system
REFERENCE 2 (bases 1 to 4032)
AUTHORS Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
TITLE TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel
JOURNAL Curr. Biol. 13 (13), 1153-1158 (2003)
PUBMED 12842017
REFERENCE 3 (bases 1 to 4032)
AUTHORS Perez,C.A., Huang,L., Rong,M., Kozak,J.A., Preuss,A.K., Zhang,H., Max,M. and Margolskee,R.F.
TITLE A transient receptor potential channel expressed in taste receptor cells
JOURNAL Nat. Neurosci. 5 (11), 1169-1176 (2002)
PUBMED 12368808
REMARK GeneRIF: functions as a cationic channel that is gated when internal calcium stores are depleted and may be responsible for capacitative calcium entry in taste receptor cells that respond to bitter and/or sweet compounds.
REFERENCE 4 (bases 1 to 4032)
AUTHORS Paulsen,M., El-Maarri,O., Engemann,S., Stroedicke,M., Franck,O., Davies,K., Reinhardt,R., Reik,W. and Walter,J.
TITLE Sequence conservation and variability of imprinting in the Beckwith-Wiedemann syndrome gene cluster in human and mouse
JOURNAL Hum. Mol. Genet. 9 (12), 1829-1841 (2000)
PUBMED 10915772
REFERENCE 5 (bases 1 to 4032)
AUTHORS Enklaar,T., Esswein,M., Oswald,M., Hilbert,K., Winterpacht,A., Higgins,M., Zabel,B. and Prawitt,D.
TITLE Mtr1, a novel biallelically expressed gene in the center of the mouse distal chromosome 7 imprinting cluster, is a member of the Trp gene family

JOURNAL Genomics 67 (2), 179-187 (2000)
PUBMED [10903843](#)
REFERENCE 6 (bases 1 to 4032)
AUTHORS Yatsuki,H., Watanabe,H., Hattori,M., Joh,K., Soejima,H., Komoda,H.,
Xin,Z., Zhu,X., Higashimoto,K., Nishimura,M., Kuratomi,S.,
Sasaki,H., Sakaki,Y. and Mukai,T.
TITLE Sequence-based structural features between Kvlqt1 and Tapal on
mouse chromosome 7F4/F5 corresponding to the Beckwith-Wiedemann
syndrome region on human 11p15.5: long-stretches of unusually well
conserved intronic sequences of kvlqt1 between mouse and human
JOURNAL DNA Res. 7 (3), 195-206 (2000)
PUBMED [10907850](#)
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from [AJ271092.2](#).
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ORIGIN

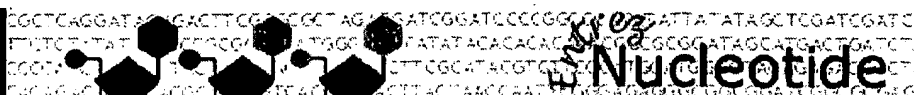
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[Details](#)

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☐ CDD

☒ MGC ☐ HPRD

☐ 1: [AJ271092](#). Reports ...[gi:8546859] The record has been replaced by [AJ271092.2](#)

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 ACCESSION AJ271092
 VERSION AJ271092.1 GI:8546859
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 4691)
 AUTHORS Paulsen,M., El-Maarri,O., Engemann,S., Stroedicke,M., Franck,O.,
 Davies,K., Reinhardt,R., Reik,W. and Walter,J.
 TITLE Sequence conservation and variability of imprinting in the
 beckwith-wiedemann syndrome gene cluster in human and mouse
 JOURNAL Hum. Mol. Genet. 9 (12), 1829-1841 (2000)
 MEDLINE 20377495
 REFERENCE 2 (bases 1 to 4691)
 AUTHORS Stroedicke,M.
 TITLE Direct Submission
 JOURNAL Submitted (14-JAN-2000) Stroedicke M., T.A.Trautner,
 Max-Planck-Institut fuer Molekulare Genetik, Ihnestrassse 73, 14195
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GenBank

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all to file

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to end

☐ Reverse complemented strandFeatures: ☐ SNP ☐ CDD☒ MGC ☐ HPRD☐ 1: [AF177473](#). Reports *Homo sapiens* MTR1...[gi:6715116]

Links

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 VERSION AF177473.1 GI:6715116
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 ORGANISM *Homo sapiens*
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 Hominidae; *Homo*.
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 AUTHORS Prawitt,D., Enklaar,T., Klemm,G., Gartner,B., Spangenberg,C.,
 Winterpacht,A., Higgins,M., Pelletier,J. and Zabel,B.
 TITLE Identification and characterization of MTR1, a novel gene with
 homology to melastatin (MLSN1) and the trp gene family located in
 the BWS-WT2 critical region on chromosome 11p15.5 and showing
 allele-specific expression
 JOURNAL Hum. Mol. Genet. 9 (2), 203-216 (2000)
 PUBMED [10607831](#)
 REFERENCE 2 (bases 1 to 3913)
 AUTHORS Prawitt,D., Pelletier,J. and Zabel,B.U.
 TITLE Direct Submission
 JOURNAL Submitted (13-AUG-1999) Children's Hospital, University of Mainz,
 Langenbeckstr. 1, Mainz, D 55101, Germany
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301	agcacaggag	cctggatcct	gaccagtgcc	ctccgcgtgg	gcctggccag	gcatgtcggg
361	caggccgtgc	gcgaccactc	gctggccagc	acgtccacca	aggtccgtgt	ggttgctgtc
421	ggcatggcct	cgctggggcg	cgctctgcac	cgccgcattc	tggaggaggc	ccaggaggat
481	tttctgttcc	actaccctga	ggatgacggc	ggcagccagg	gccccctctg	ttcactggac
541	agcaacctct	cccacttcat	cctggtggag	ccaggcccc	cggggaaggg	cgatgggctg
601	acggagctgc	ggctgaggct	ggagaagcac	atctcggagc	agagggcggg	ctacgggggc
661	actggcagca	tcgagatccc	tgtcctctgc	ttgctggtca	atggtgatcc	caacaccttg
721	gagaggatct	ccaggggcgt	ggagcaggct	gccccgtggc	tgatcctggt	aggctcgggg
781	ggcatcgccg	atgtgcttgc	tgccctagt	aaccagcccc	acctcctggt	gccaagggtg
841	gccgagaagc	agtttaagga	gaagtccccc	agcaagcatt	tctcttgga	ggacatcgtg
901	cgctggacca	agctgctgca	gaacatcacc	tcacaccagc	acctgctcac	cgtgtatgac
961	ttcgagcagg	agggctccga	ggagctggac	acggctcatc	tgaaggcgct	ggtgaaagcc
1021	tgcaagagcc	acagccagga	gcctcaggac	tatctggatg	agctcaagct	ggccgtggcc
1081	tgggaccgcg	tggacatcgc	caagagtgcg	atcttcaatg	gggacgtgga	ggcgaagctc
1141	tgtgacctgg	aggaggtgat	ggtggacgcc	ctggtcagca	acaagcccga	gtttgtgcgc
1201	ctctttgtgg	acaacggcgc	agacgtggcc	gacttcctga	cgtatgggcg	gctgcaggag
1261	ctctaccgct	ccgtgtcacg	caagagcctg	ctcttcgacc	tgctgcagcg	gaagcaggag
1321	gaggcccggc	tgacgctggc	cggcctgggc	accagcagg	cccgggagcc	accgcggggg
1381	ccaccggcct	tctccctgca	cgaggtctcc	cgcgactca	aggacttctt	gcaggacgcc
1441	tgccgaggct	tctaccagga	cggccggcca	ggggaccgca	ggagggcgga	gaagggcccc
1501	gccaagcggc	ccacgggcca	gaagtggctg	ctggacctga	accagaagag	cgagaacccc
1561	tggcgggacc	tgttcctgtg	ggccgtgctg	cagaaccgcc	acgagatggc	cacctacttc
1621	tgggccatgg	gccaggaagg	tgtggcagcc	gcaactggcg	cctgcaaat	cctcaagag
1681	atgtcgcacc	tggagacgga	ggccgaggcg	gcccagacca	cgcgcgaggc	gaaatacgag
1741	cggctggccc	ttgacctctt	ctccgagtgc	tacagcaaca	gtgaggcccc	cgcttcgcc
1801	ctgctggtgc	gccggaaccg	ctgctggagc	aagaccacct	gcctgcacct	ggccaccgag
1861	gctgacgcca	aggccttctt	tgcccacgac	ggcggtcagg	ccttcctgac	caggatctgg
1921	tggggggaca	tggccgcagg	cacgcccatt	ctgcggctgc	taggagcctt	cctctgcccc
1981	gccctcgtct	ataccaacct	catcaccttc	agtgaggaag	ctcccctgag	gacaggcctg
2041	gaggacctgc	aggacctgga	cagcctggac	acggagaaga	gcccgtgta	tggcctgcag
2101	agccgggtgg	aggagctggt	ggaggcgccg	agggctcagg	gtgaccgagg	cccacgtgct
2161	gtcttcctgc	tcacacgctg	gcggaatttc	tggggcgctc	ccgtgactgt	gttctctggg
2221	aacgtggtca	tgtacttcgc	cttcctcttc	ctgttcacct	acgtcctgct	ggtggacttc
2281	aggccgcccc	cccaggggcc	ctcaggggcc	gaggtcaccc	tctacttctg	ggtctttacg
2341	ctggtgctgg	aggaaatccg	gcagggcttc	ttcacagacg	aggacacaca	cctggtgaag
2401	aagttcacac	tgtatgtggg	ggacaactgg	aacaagtgtg	acatggtggc	catcttctctg
2461	ttcatcgtgg	gtgtcacctg	caggatgctg	ccgtcggcgt	ttgaggctgg	ccgcacggctc
2521	ctcgccatgg	acttcatggt	gttcacgctg	cggctgatcc	atatctttgc	catacacaag
2581	cagctggggc	ccaagatcat	cgtggtagag	cgcatgatga	aggacgtctt	cttcttcctc
2641	ttctttctga	gcgtgtggct	cgtggcctac	ggtgtcacca	cccaggcgct	gctgcacccc
2701	catgacggcc	gcctggagt	gatcttcgcg	cgggtgctct	accggcccta	cctgcagatc
2761	ttcgccaga	tcccactgga	cgagattgat	gaagcccgtg	tgaactgctc	caccacccca
2821	ctgctgctgg	aggactcacc	atcctgcccc	agcctctatg	ccaactggct	ggtcatcctc

```
2881 ctgctgggtca ccttcctggt ggtcaccaat gtgctgctca tgaacctgct catcgccatg
2941 ttcagctaca cgttccaggt ggtgcagggc aacgcagaca tgttctggaa gttccagcgc
3001 tacaacctga ttgtggagta ccacgagcgc cccgccctgg ccccgccctt catcctgctc
3061 agccacctga gcctgacgct ccgccgggtc ttcaagaagg aggctgagca caagcgggag
3121 cacctggaga gagacctgcc agacccctg gaccagaagg tcgtcacctg ggagacagtc
3181 cagaaggaga acttcctgag caagatggag aagcggagga gggacagcga gggggagggtg
3241 ctgcggaata ccgcccacag agtggacttc attgccaagt acctcggggg gctgagagag
3301 caagaaaagc gcatcaagtg tctggagtca cagatcaact actgctcggt gctcgtgtcc
3361 tccgtggctg acgtgctggc ccagggtggc ggcccccgga gctctcagca ctgtggcgag
3421 ggaagccagc tgggtggctgc tgaccacaga ggtgggttag atggctggga acaaccggg
3481 gctggccagc ctccctcgga cacatgagct gcttggcctg ccacgtgtgg ggccacctct
3541 cttcagttgg ccacctgca cgttgtgcac tgacctttgc cgacctccag cggaaacccc
3601 cagggggcac cagcccccca gcagacaatg gccctcctgg tgcctacca cagacctca
3661 cccaaaggaa ccgctccttg tccctcctgg cctccccgga ggcacagcag tgtcatgggg
3721 ctgtctcccc tgacaggcac aactccccgg gcagaaaacg tgccccaccg catccctacc
3781 tggaaactga ccagcctgca ctgtggaaaa gctggccctg tggcgtgacg ggggagcacc
3841 cccatccaga ctgcgaagct gctctgggtc tgcaccacc cctgccctga cttgtgttgc
3901 ctgacaagag act
```

//

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Feb 9 2005 14:31:10

Align two sequences

Tue Mar 1 21:52:38 "GMT 2005

```
/usr/tmp/seq1.73316.sca : 1158 aa
>Mouse MTR1, 1158 bases, 31D4F27D checksum.      1158 aa vs.
>Human MTR1, 1165 bases, C1D16397 checksum.      1165 aa
scoring matrix: , gap penalties: -12/-2
84.1% identity;      Global alignment score: 6543
```

```
      10      20      30      40      50      60
/usr/t MQTTQSSCPGSPPDTEGWEPILCRGEINFGGSGKKRGKFKVVPSSVAPSVLFELLTEW
      :: ...  :::: :::: : : ::::::::::::::::::::::::::::::::::::::
Human  MQDVQGP RP GSPGDAEDRRELGLHRGEVNF GGSGKKRGKFKVRVPSGVAPSVLFDLLAEW
      10      20      30      40      50      60

      70      80      90     100     110     120
/usr/t HLPAPNLVSVSLVGEE RPLAMKSWLRDVL RKGLV KAAQSTGAWILTSALHVGLARHVGQAV
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Human  HLPAPNLVSVSLVGEE QPFAMKSWLRDVL RKGLV KAAQSTGAWILTSALRVGLARHVGQAV
      70      80      90     100     110     120

      130     140     150     160     170     180
/usr/t RDHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDTPIHYPADENIQGPLCPLDS
      ::::::::::::::::::::::: ::::: . .: ::::: ::::: ::::: :::::
Human  RDHSLASTSTKVRVAVGMASLGRVLHRRILE--EAQEDFPVHYPEDDGGSQGPLCSLDS
      130     140     150     160     170

      190     200     210     220     230     240
/usr/t NLSHFILVESGALGSGNDGLTELQLSLEKHISQORTGYGGTSCIQIPVLCLLVNGDPNTL
      ::::::::::: : :: ::::::::::: ::::::::::: ::::::::::: ::::::::::
Human  NLSHFILVEPGPPGKG-DGLTELRLRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTL
      180     190     200     210     220     230

      250     260     270     280     290     300
/usr/t ERISRAVEQAAPWLILAGSGGIADVLAALVSQPHLLVPQVAEKQFREKFPSECF SWEAIV
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::: :::::
Human  ERISRAVEQAAPWLILVSGSGGIADVLAALVNQPHLLVPKVAEKQFKEKFP SKHFSWEDIV
      240     250     260     270     280     290

      310     320     330     340     350     360
/usr/t HWTELLQNIAAHPHLLTVYDFEQEGSELDLTVILKALVKACKSHSQEAQDYLDLKLAVA
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
Human  RWTKLLQNITSHQHLLTVYDFEQEGSELDLTVILKALVKACKSHSQEPQDYLDLKLAVA
      300     310     320     330     340     350

      370     380     390     400     410     420
/usr/t WDRVDIAKSEIFNGDVEWKSCDLEEVMTDALVSNKPDFVRLFVDSGADMAEFLTYGRLQQ
      ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
Human  WDRVDIAKSEIFNGDVEWKSCDLEEVMTDALVSNKPEFVRLFVDNGADVADFLTYGRLQE
      360     370     380     390     400     410

      430     440     450     460     470     480
/usr/t LYHSVSPKSLLFELLQRKHEEGRLTLAGLGAQQARELP IGLPAFSLHEVSRVLKDFLHDA
      ::::: ::::::::::: ::::::::::: : : ::::::::::: :::::::::::
Human  LYRSVSRKSLLFDDLQRKQEEARLTLAGLGTQQAREPPAGPPAFSLHEVSRVLKDFLQDA
      420     430     440     450     460     470
```


Sequence Alignment Output

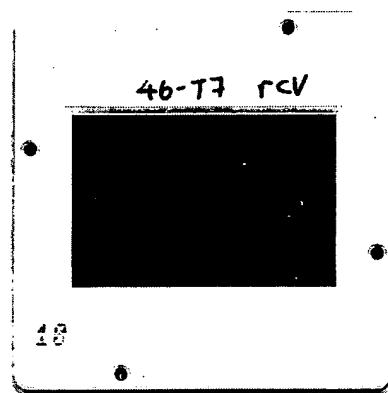
Human LRKTAHRVDFIAKYLGGLREQEKRIKCLESQINYSVLVSSVADVLAQGGGPRSSQHCGE

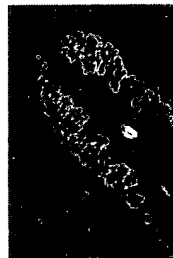
```

      1140      1150
/usr/t RSQPASARDREYLE-----SGLPPSDT
      :: ..: : : . : : ::
Human  GSQLVAADHRGGGLDGWEQPGAGQPPSDT
      1140      1150      1160

```

Elapsed time: 0:00:00





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